

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2003, 10:15:28 ; Search time 37.8045 Seconds
(without alignments)
8639.474 Million cell updates/sec

Title: US-09-922-895-2

Perfect score: 1065

Sequence: 1 ATGACAACTCTAGATAC.....CGAAGCTCTATGTTT 1065

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA: *
1: /cgn2_6/ptodata/1/lna/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/lna/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/lna/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/lna/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/lna/PCIVS.COMB.seq: *
6: /cgn2_6/ptodata/1/lna/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1065	100.0	1065	US-08-847-296B-2	Sequence 2, Appl1
2	1065	100.0	1915	US-08-575-967A-3	Sequence 3, Appl1
3	540.8	50.8	2156	US-08-012-988A-1	Sequence 1, Appl1
4	363.4	34.1	1059	US-08-724-984A-3	Sequence 3, Appl1
5	363.4	34.1	1376	US-09-087-232A-12	Sequence 12, Appl1
6	363.4	34.1	1477	US-08-833-752-2	Sequence 2, Appl1
7	363.4	34.1	3383	US-08-861-105-13	Sequence 13, Appl1
8	363.4	34.1	3383	US-08-575-967A-1	Sequence 1, Appl1
9	363.4	34.1	5674	US-09-293-170-3	Sequence 3, Appl1
10	361.8	34.0	1071	US-09-087-232A-14	Sequence 14, Appl1
11	361.8	34.0	1414	US-08-466-343D-1	Sequence 1, Appl1
12	360.6	33.9	1059	US-09-517-605-8	Sequence 8, Appl1
13	360.6	33.9	2440	US-08-724-984A-1	Sequence 1, Appl1
14	348.8	32.8	1979	US-08-450-393A-3	Sequence 3, Appl1
15	348.8	32.8	1979	US-08-446-669-3	Sequence 3, Appl1
16	348.8	32.8	1979	PCT-US95-00476-3	Sequence 3, Appl1
17	323.4	30.4	2232	US-08-450-393A-1	Sequence 1, Appl1
18	323.4	30.4	2232	US-08-446-669-1	Sequence 1, Appl1
19	323.4	30.4	2232	PCT-US95-00476-1	Sequence 1, Appl1
20	318.2	29.9	1344	US-09-087-232A-16	Sequence 16, Appl1
21	318.2	29.9	1442	US-08-833-752-3	Sequence 3, Appl1
22	259.2	24.3	1607	US-08-875-573-19	Sequence 19, Appl1
23	259.2	24.3	1695	US-09-232-878-1	Sequence 1, Appl1
24	235.6	22.1	1161	US-08-153-848-31	Sequence 31, Appl1
25	235.6	22.1	1161	PCT-US93-11153-31	Sequence 31, Appl1
26	235.6	22.1	2254	US-08-153-848-27	Sequence 27, Appl1
27	235.6	22.1	2254	US-09-299-843A-27	Sequence 27, Appl1

28	235.6	22.1	2254	US-09-088-337B-27	Sequence 27, Appl1
29	235.6	22.1	2254	PCT-US93-11153-27	Sequence 27, Appl1
30	235.6	22.1	3119	US-09-299-843A-31	Sequence 31, Appl1
31	235.6	22.1	3119	US-09-088-337B-31	Sequence 31, Appl1
32	221.2	20.8	1586	US-08-461-244-1	Sequence 1, Appl1
33	206.6	19.4	792	US-08-833-752-1	Sequence 1, Appl1
34	198.2	18.6	1050	US-08-681-192-1	Sequence 1, Appl1
35	178.2	16.7	461	US-09-087-232A-11	Sequence 11, Appl1
36	170.4	16.0	1510	US-07-759-568-4	Sequence 4, Appl1
37	170.4	16.0	1748	US-08-202-056-8	Sequence 8, Appl1
38	167.8	15.8	1900	US-08-153-848-18	Sequence 18, Appl1
39	167.8	15.8	1900	US-09-299-843A-18	Sequence 18, Appl1
40	167.8	15.8	1900	US-09-088-337B-18	Sequence 18, Appl1
41	167.8	15.8	1900	PCT-US93-11153-18	Sequence 18, Appl1
42	167.8	15.8	2058	US-08-153-848-6	Sequence 6, Appl1
43	167.8	15.8	2058	US-09-299-843A-6	Sequence 6, Appl1
44	167.8	15.8	2058	US-09-088-337B-6	Sequence 6, Appl1
45	167.8	15.8	2058	PCT-US93-11153-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-08-847-296B-2
; Sequence 2, Application US/08847296B
; Patent No. 6271347
; GENERAL INFORMATION:
; APPLICANT: DAUGHERTY, BRUCE L.
; APPLICANT: DEMARTINO, JULIE A.
; APPLICANT: SICILIANO, SALVATORE J.
; APPLICANT: SPRINGER, MARTIN J.
; TITLE OF INVENTION: EOSINOPHIL EOTAXIN RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P. O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,296B
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/016,158
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 60/017,113
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Thies, J. Eric
; REGISTRATION NUMBER: 35,382
; REFERENCE/DOCKET NUMBER: 19634Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3904
; TELEFAX: 908-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1065 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-847-296B-2
Query Match 100.0%; Score 1065; DB 4; Length 1065;

QY	301	TTTGGCCATGGCAATGCTTAGCTCTCTCAGGGTTTATCACACAGGGCTTTGACAGCGA3	360
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QY	361	ATCTTTTCAATATCCGCTGACAAATGCAGAGGTACCTGGCCATTGCTCATCTGTGTT	420
Db	722	ATCTTTTCAATATCCGCTGACAAATGCAGAGGTACCTGGCCATTGCTCATCTGTGTT	781
QY	421	GCCCTTGAGCCCGGACTGTCTATTTGGTGTCATCAGCAGCATGCTACCTGGGGCCTG	480
Db	782	GCCCTTGAGCCCGGACTGTCTATTTGGTGTCATCAGCAGCATGCTACCTGGGGCCTG	841
QY	481	GCACTGCTAGCAGCTCTCTCTGAATTTATCTTATAGACATGAGAGTGTGTTGAAG	540
Db	842	GCACTGCTAGCAGCTCTCTCTGAATTTATCTTATAGACATGAGAGTGTGTTGAAG	901
QY	541	ACCTTTTGACAGTGCTCTTTACCCAGAGGATACGATATAGCTGGAGGATTTCCACACT	600
Db	902	ACCTTTTGACAGTGCTCTTTACCCAGAGGATACGATATATAGCTGGAGGATTTCCACACT	961
QY	601	CTGAGAAATGACATCTTCTGTCCTGTTCTCCCTCTGCTGTTATGGCCATCTGTACACA	660
Db	962	CTGAGAAATGACATCTTCTGTCCTGTTCTCCCTCTGCTGTTATGGCCATCTGTACACA	1021
QY	661	GGAATCATCAAAAGCGCTGCTGAGGTGCCCGCAGTAAAAAAAGTACAGGCCATCCGGCTC	720
Db	1022	GGAATCATCAAAAGCGCTGAGGTGCCCGCAGTAAAAAAAGTACAGGCCATCCGGCTC	1081
QY	721	ATTTTGTGATCATGAGCGGGTGTTCATTTTGTGACACCCATCAATGGCTATCCCT	780
Db	1082	ATTTTGTGATCATGAGCGGGTGTTCATTTTGTGACACCCATCAATGGCTATCCCT	1141
QY	781	CTCTCTTCATCAATCATCTTATTTGGAAATGACTGTGAGCGGAGCAAGCATCTGAGC	840
Db	1142	CTCTCTTCATCAATCATCTTATTTGGAAATGACTGTGAGCGGAGCAAGCATCTGAGC	1201
QY	841	CTGCTGATGCTGCTGAGACAGAGTGATCGCTACTCCCATCTGCTGCAATGAACCCGGTGATC	900
Db	1202	CTGCTGATGCTGCTGAGACAGAGTGATCGCTACTCCCATCTGCTGCAATGAACCCGGTGATC	1261
QY	901	TACGCCTTTGTGGAGAGAGGTTCCGGAATACCTCGGCACCTTCTCCAGAGGCACCTG	960
Db	1262	TACGCCTTTGTGGAGAGAGGTTCCGGAATACCTCGGCACCTTCTTCCACAGGCACCTTG	1322
QY	961	CTCATGACACCTGGGACAGATACATCCATTCTTCTCATGTAGAGAGCTGGAAAGAACACAC	1020
Db	1322	CTCATGACACCTGGGACAGATACATCCATTCTTCTCATGTAGAGAGCTGGAAAGAACACAC	1381
QY	1021	TCTGTCTCTCATTCACACGACGAGCCGGAACTCTATTTGTGTTT	1065
Db	1382	TCTGTCTCTCATTCACACGACGAGCCGGAACTCTATTTGTGTTT	1426
RESULT 3			
US-08-012-988A-1			
: Sequence 1, Application US/08012988A			
: Patent No. 5652133			
: GENERAL INFORMATION:			
: APPLICANT: Murphy, Philip M.			
: TITLE OF INVENTION: Cloning and Expression of Human			
: TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1			
: NUMBER OF SEQUENCES: 2			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: Townsend and Townsend Kourile and Crew			
: STREET: One Market Plaza, Steuart Tower, Suite 2000			
: CITY: San Francisco			
: STATE: California			
: COUNTRY: USA			
: ZIP: 94610			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: COMPUTER: IBM PC compatible			
:			

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/012,988A
FILING DATE: 19930128
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weber,, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15280-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2156 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: primer_bind
LOCATION: 259..275
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1
FEATURE:
NAME/KEY: complement (868..884)
LOCATION: 1
FEATURE:
NAME/KEY: CDS
LOCATION: 63..1128
US-08-012-988A-1

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Query Match	50.88;	Score	540.8;	DB	1;	Length	2156;
Best Local Similarity	69.38;	Pred	No. 3.4e-140;				
Matches	737;	Conservative	0;	Mismatches	327;	Indels	0;
				Gaps			
Qy	1	ATGCAACCTTCATGATACGTTGAGACCTTTGGTACCAATCCATCTATATGATACGTG	60				
Db	63	ATGGAAACTCCAAACACACAGAGAGCATATGACACGACACAGAGTTTGACTATGGGGAT	1222				
Qy	61	GGCCTGCTGTGAAAAGCGATACAGAGCACTGATGGCCCGCATTTGGCCCCCGCTG	1200				
Db	123	GCAACTCCGTCGCGAAGAGGTGACGAGAGGGCCTTTTGGGGCCCACTGTGCCCCCTTG	1822				
Qy	121	TACTCCCTGCTGTTCACTGTGGGCTCTTGGGCAATGTGGTGTGATGATTCCTATA	1800				
Db	183	TACTCCTTGGTATTTGTCATTTGGCCTGTTGGAAACAATCCTGGGGTCTGTGCTCTGTG	2422				
Qy	181	AAATACAGAGAGCTCGCAATATATGACCAACATCTACTGCTCAACCTGGGCATTTTGGAC	2400				
Db	243	CAATACAGAGAGCTTAAAAAACATGACAGACATCTACTCTGAAACCTGGGCATTTTCTGAC	3020				
Qy	241	CTGCTCTCCGTCGTCACCCCTTCCATTTCTGTGATCCACTATGTCAGAGGGGCACTTAATCTGGTT	3000				
Db	303	CTGCTCTCCGTTCCAGGCTTCCCTTCTGGATGCACTAACAAGTTGAAGATGATCGGCTT	3622				
Qy	301	TTTGGCCATGCGATGTAAAGTCTCTCAAGGCTTTTATCACAGAGCTTGTACAGCGAG	3600				
Db	363	TTTGGTATGCGATGTAAAGTCTCTCGGGGTTTATACACAGGCTTGTACAGCGAG	4222				
Qy	361	ATCTTTTTCATATTCGTCGTCGACATGACAGAGTACCTGGCATTTGCAATGCTGTTT	4200				
Db	423	ATCTTTTTCATATTCGTCGTCGACATTTGACAGTACTGGGCATCTGTACAGCCGTGTTT	4822				
Qy	421	GGCCTTGAGCCGGGACTGTCACTTTTGTGTGTCATCACACAGATGTCACCTGGGGCTTG	4800				
Db	483	GGCTTGGGGGACCGACCGTCACATTTTGGTGTCAATCACAGCATCAATTTTGGGCCCTTG	5422				
Qy	481	GCATGTGCAGACGCTTCTCCGATTTATCTCATAGAGACTGAAGGATTGTTTGAAGAG	5400				
Db	543	GGCATCTTGGCTTTCATGCGCAGGCTTATCTTTTCCAAAGACCCATGGAATTCATCTCAC	6020				
Qy	541	ACTCTTTCGACGTGCTTTTAAACCGAGAGATACAGTATATAGCTGGAGGCAATTTTCACACT	6000				

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Db 603 CACACGTGACGCTTCACTTCTCTCACGAAAGCCTACGAGAGTGAAGCTGTTCAGGCT 662
Qy 601 CTGAGATGACCATCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
Db 663 CTGAACTGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 722
Qy 661 GGAATCATCAAAAGCGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 723 GGAATTTAAAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 782
Qy 721 ATTTTGTATCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 783 ATTTTGTATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 842
Qy 781 CTCTCTCCATCATCATCATCTTATTTGGAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 843 ATTTCTGTTTCCAAAGCTTCTCTTCAACCATATGCTGCTGCTGCTGCTGCTGCTGCTGCT 902
Qy 841 CTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 903 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 962
Qy 901 TACGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 963 TACGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1022
Qy 961 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 1023 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1082
Qy 1021 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1064
Db 1083 TCCACATCTCCCTCCACAGGAGCATGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1126

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RESULT 4
 US-08-724-984A-3
 ; Sequence 3, Application US/08724984A
 ; Patent No. 6388055
 ; GENERAL INFORMATION:
 ; APPLICANT: Derek Bergsma, Mary Brawner, and Usman Shabon
 ; TITLE OF INVENTION: NO. 6388055el Mouse Genomic Clone of the CC-
 ; NUMBER OF INVENTION: CKR5 Receptor
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corporation
 ; STREET: 709 Swedeland Road, P.O. Box 1539
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406-0939
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
 ; COMPUTER: IBM 486
 ; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
 ; SOFTWARE: MICROSOFT WORD
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/724,984A
 ; FILING DATE: October 3, 1996
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: William T. Han
 ; REGISTRATION NUMBER: 34,344
 ; REFERENCE/DOCKET NUMBER: ATG50023
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610 270 5024
 ; TELEFAX: 610 270 5090
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1059

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; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: No
; US-08-724-984A-3

Query Match      34.1%; Score 363.4; DB 4; Length 1059;
Best Local Similarity 62.2%; Pred. No. 3.2e-91;
Matches 625; Conservative 0; Mismatches 371; Indels 9; Gaps 3;

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Db 603 CACACGTGACGCTTCACTTCTCTCACGAAAGCCTACGAGAGTGAAGCTGTTCAGGCT 662
 Qy 601 CTGAGATGACCATCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
 Db 663 CTGAACTGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 722
 Qy 661 GGAATCATCAAAAGCGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 Db 723 GGAATTTAAAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 782
 Qy 721 ATTTTGTATCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 Db 783 ATTTTGTATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 842
 Qy 781 CTCTCTCCATCATCATCATCTTATTTGGAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 Db 843 ATTTCTGTTTCCAAAGCTTCTCTTCAACCATATGCTGCTGCTGCTGCTGCTGCTGCTGCT 902
 Qy 841 CTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 Db 903 CTGCT 962
 Qy 901 TACGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 Db 963 TACGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1022
 Qy 961 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 Db 1023 GCT 1082
 Qy 1021 TCTGCT 1064
 Db 1083 TCCACATCTCCCTCCACAGGAGCATGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1126

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-861-105-13

Query Match 34.1%; Score 363.4; DB 4; Length 3383;
Best Local Similarity 62.2%; Pred. No. 5.2e-91;
Matches 625; Conservative 0; Mismatches 371; Indels 9; Gaps 3;

66 GCCTGTGAAAAAGCTGATACCAAGACACTGATGCCCCAGTTGGCCCCGTGACTC 135
108 GCCCTGCAAAATATGAGCAAAATGCGAGCCGCTCCTGCTGCTGCTGCTC 167
126 CCGTGTGATGATGAGGCTCTGGGCAATGAGTGGTGTATGATGATCTCTAATAA 165
168 ACTGCTGATCTTTGGTTTGTGGCAACATGCTGCTATCTCTCATCTGATAAACTG 227
186 CAGAGGCTCCGATATGACCAACATCTACCTGCTCAACCTGGCCATTTGCGACCTGCT 245
228 CAAAGGCTGAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 287
246 CTTCCTGCTACCTCTTCATCTGATGATGATGATGATGATGATGATGATGATGATGAT 305
288 TTTCCTTCTTACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 344
306 CCATGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 365
345 AATATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 404
366 TTTCATATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 425
405 CTTCATCATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 464
426 TCGAGCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 485
465 AAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 524
486 GCTGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 545
525 GTTGGCTCTCTCCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 564
546 TTGCACTGCTCTTACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 605
585 CTGACCTCTCATCTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 644
606 AATGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 665
645 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 704
666 CATCAAAAGCTGCTGAGTGGCCCACT---AAAAAAGTAAAGGCTTCCGGCTCAT 722
705 CCTAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 764
723 TTTCATATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 782
765 CTTCATCATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 824
783 CTTCCTTCTTACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 842
825 GAACACTCTTCCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 884
843 GGTCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 902
885 AGCTATGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 944
903 CCGCTTTGAGAGAGTTCGGAAGTACCTGCGCACTCTCTCTCACAGGACCTTGGT 962
945 TGGCTTTGTCGGGGAAGATTCAGAAACTACCTTAGTCTTCTCCAAAGACATTTG 1004
963 CATGACCTGGGAGATACATCCATCTCTCTAGTGAAGAGCTGGAAGAACACAGCTTC 1022

1005 CAAAGCTTCTGCAAAATGCTGTTCTATTTCCAGCAAGAGCTGCCAGGAGCAAGCTC 1064
1023 TGT---CTTCATATCCACAGAGCGCGGAACTCTCTATGTGTT 1064
1065 AGTTTACCCGATCCACTGCGGAGGAGAAATATCTGTGGCTT 1109

RESULT 8

US-08-575-967A-1
Sequence 1, Application US/08575967A

Patent No. 6265184

GENERAL INFORMATION:

APPLICANT: Gray et al.

TITLE OF INVENTION: Chemokine Receptor Materials and Methods

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/575,967A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: No. 6265184 and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 32918

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-485-1662

TELEFAX: 206-485-1662

INFORMATION FOR SEQ. ID NO. 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3383 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 55..1110

FEATURE:

NAME/KEY: misc. feature

OTHER INFORMATION: /- "88C polynucleotide and amino acid

US-08-575-967A-1

Query Match 34.1%; Score 363.4; DB 4; Length 3383;
Best Local Similarity 62.2%; Pred. No. 5.2e-91;

Matches 625; Conservative 0; Mismatches 371; Indels 9; Gaps 3;

66 GCCTGTGAAAAAGCTGATACCAAGACACTGATGCCCCAGTTGTGCCCCGTGACTC 125
108 GCCCTGCAAAATATGAGCAAAATGCGAGCCGCTCCTGCTGCTGCTGCTGCTGCT 167
126 CCGTGTGATGATGAGGCTCTGGGCAATGAGTGGTGTATGATGATCTCTAATAA 185
168 ACTGCTGATCTTTGGTTTGTGGCAACATGCTGCTATCTCTCATCTGATAACTG 227
186 CAGAGGCTCCGATATGACCAACATCTACCTGCTCAACCTGGCCATTTGCGACCTGCT 245
228 CAAAGGCTGAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 287
246 CTTCCTGCTACCTCTTCATCTGATGATGATGATGATGATGATGATGATGATGATGAT 305
288 TTTCCTTCTTACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 344

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QY 306 CCATGGCATGTGTAACTCTCTCAGGGTTTATATACAGAGCGTTGTACAGCAGATCTT 365
      || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 345 AATATACATGTGTCACTCTTGACAGGGCTATTTATAGGCTTCTCTGATCTT 404
QY 366 TTTCATATCTCTGCTACATGACAGGTAACCTGGCCATTGCTCAGCTGTGTTGCCCT 425
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 405 CTTCATCATCTCTCTACATCATGATGACCTGGCTGCTGCTGCTGCTGCTGCTGCTT 464
QY 426 TCGAGCCCGGACGTGACATTTTGGTGTACATCAGCATGCTGACCGGGGGCTGACAG 485
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 465 AAAAGCAGAGCGTACCTTTGGGGGTGACAAAGTGTATCATCTGGGTGGGTGCTG 524
QY 486 GCTAGACGCTCTCTCTGAAATTTATCTTATGAGACTGAGAGTTTGAAGAGACTCT 545
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 525 GTTTGGGTCTCTCCAGGATCATCTTTACCAATCTCAAAAAGAGTCTTATTAACAC 584
QY 546 TTGCACTGCTCTTTACCCAGAGATATATATAGCTGGAGCATTTCCACACTGTAG 605
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 585 CTGACGCTCTCATTTTCCATACAGTATCATATCTGGAAGAAATTTCCAGACATTTAA 644
QY 606 AATGACATCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 665
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 645 GATAGTATCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 704
QY 666 CATCAAAAGCGTCTGAGTGGCCAGT--AAAAAAAGTACAGAGCCATCCGCTCAT 722
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 705 CCAAAAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 764
QY 723 TTTTGTATCATGTGGGCTGTTTTCATTTCTGACACCTTACAAATGTGCTTCTCT 782
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 765 CTTCACCATCTCATTTTATTTATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 824
QY 783 CTCTTCATCATCATCTTATTTTGAATGACTGTGAGCGGAGCATCTGACCT 842
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 825 GAACACTCTTCAGGAATCTTTTGGCTGATTAATGCTAGTATGCTAAGCTGTGACCA 884
QY 843 GGTATCTGTGTGAGAGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 885 AGCTATGAGGTGAGAGAGTCTTGGGATGAGCAGTCTGCTGCTGCTGCTGCTGCTGCT 944
QY 903 CGCTTTGTGAGAGAGTTCGGGAAGTACCTGCGGCACTTTCTTCACAGGCACTTGT 962
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 945 TGCCTTTGTGGGAGAAAGTTCAGAACTGCTTATGCTTTTTCACAAAGCAGATGCT 1004
QY 963 CATGCACTGTGGAGATATCATCTCTCTTCTAGAGAGCTGGAAGAACAGCAGCTC 1022
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1005 CAACGCTTCTGCAATGCTGTCTATTTTCCAGCAAGAGCTCCGAGCGAGCAGACCTC 1064
QY 1023 TGT--CTCTCATCCAGAGAGCCGGAACCTCTATTGTGT 1064
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1065 AGTTTACACCCGATCCACTGGGAGCAGGAATATCTGTGGGCTT 1109
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RESULT 9
US-09-293-170-3
; Sequence 3, Application us/09293170
; Patent No. 6383777
; GENERAL INFORMATION:
; APPLICANT: Breyer, Richard M.
; APPLICANT: Ma, Lijun
; APPLICANT: Kennedy, Chris
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH YIELD
; TITLE OF INVENTION: PRODUCTION OF EUKARYOTIC PROTEINS
; FILE REFERENCE: 22000.0094
; CURRENT APPLICATION NUMBER: us/09/293,170
; EARLIER FILING DATE: 1999-04-16
; EARLIER APPLICATION NUMBER: 60/081,989
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 5674
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (300)...(1616)
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: synthetic construct
US-09-293-170-3

Query Match
Best Local Similarity 62.2%; Pred. No. 6.3e-91;
Matches 625; Conservative 0; Mismatches 371; Indels 9; Gaps 3;

QY 66 GCTCTGTGAAAAGCTGATACAGAGCACTGATGAGCCAGTTTGTGCCCCGCTGATCTC 125
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 587 GCCCTGCCAAAAATATATGTGAAGCAATCGAGCGCCGCTCTCTCCGCTGCTACCTC 646
QY 126 CCTGTGTCTACTGTGGGCTCTTGGGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 185
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 647 ACTGTGTCTCATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 706
QY 186 CAGAGAGCCCGCAATATATGACCAACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 245
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 707 CAAGAAGCTGAAGAGCATGATGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 766
QY 246 CTTCCTCTGTCACCCCTTCCATCTGATCCACTATGTGACAGGGGCAATAGCTGGTTTGTG 305
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 767 TTTCTCTTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 823
QY 306 CCATGCACTGTGTAACCTCTCTCAGGGTTTATATCACAGGCTTTACAGCAGATCTT 365
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Db 824 AATATACATATCTGCAACTCTGACAGGGGCTATTTTAAGGCTTCTCTGGAATCTT 883
QY 366 TTTCATATCTCTCTGACATGACAGGTAACCTGGCCATTTGCTGCTGCTGCTGCTGCTGCT 425
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Db 884 CTTCATCATCTCTCTGACATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 943
QY 426 TCGAGCCCGGACTGTGACTTTTGTGCTGATCAGCAGACATGCTGCTGCTGCTGCTGCTGCT 485
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Db 944 AAAAGCAGAGCGTACACTTTGGGGTGTGACAAAGTATGATCACTTGGGTGTGCTGCT 1003
QY 486 GTAGAGCTCTCTCTGATTTATCTTATGAGACTGGAAGTGTGTTGAAGAGCTCT 545
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Db 1004 GTTTGGGTCTCTCCAGGATCATCTTTACAGATCTCAAAAAGAGTCTTCTATTACAC 1063
QY 546 TTGCAAGTCTTTTACCAAGAGATACAGTATATAGCTGGAGGCACTTTCACACTGTAG 605
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Db 1064 CTGCACTCTCATTTTTCATACAGTACATGATCAATTTCTGGAAGAAATTTCCAGCATTTAA 1123
QY 606 AATGACCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 665
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1124 GATAGTATCTTGGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1183
QY 666 CATCAAAAGCGTCTGAGTGGCCAGT--AAAAAAAGTACAAAGCCATCCGCTCAT 722
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1184 CCAAAAAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1243
QY 723 TTTTGTATCATGTGGGCTGTTTTCATTTTCTGACACCTTACAAATGTGCTATCTCTCT 782
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Db 1244 CTTCACCATCTATTTTATTTTATTTTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1303
QY 783 CTCTTCATCATCATCTTATTTTGAATGACTGTGAGCGGAGCAGCAGCATCTGAGCT 842
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1304 GAACACTCTTCAGGAATCTTGGGCTGATTAATGAGTCAAGTCAACAGTGTGAGACA 1363
QY 843 GGTATCTGTGTGAGAGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1364 AGTATGAGGTGACAGAGTCTTGGGATGAGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 1423
QY 903 CGCTTTGTGAGAGAGTTCGGGAAGTATCTGCGGCACTTCTTCACAGGCACTTGTCT 962
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1424 TGCCTTTGTGGGAGAGTTCAGAAACTGCTTATGCTTCTTCCAAAAGCAGCATTTGC 1483
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DB 1354 CAGGGCTGTGAGGCTCATCTTGGCATCATGATTTGCTACTTCTCTCGACCTCCCTA 1413
QY 765 CATATGGCTATCCCTCTCTCTCTCCATCATCATCCATCTATTGGAAAGACGTGAGG 824
DB 1414 CACATCTGCTCTCTCTCTCAACACCTTCCAGGAACTTTGGACATGAAATGACAGT 1473
QY 825 GAGCAGCATCTGAGCCTGTCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 884
DB 1474 TTCTATATACATGACACGACGACATGACAGGACCTTTGGAAATGACACACTGCTG 1533
QY 885 CATGAACCCGGTATCTACGCTTTTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 944
DB 1534 CCAAAACCTGTATCTATGCTTTTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1593
QY 945 CTTCCAGAGGACCTTGTCTGATGACCTGGGAGATACATCCATCTCTCTCTATGAGA 1004
DB 1594 CTTCCAGAGGACCTTGTCTGATGACCTGGGAGATACATCCATCTCTCTATGAGA 1653
QY 1005 GCTGGAAGAGACGCTCTGTCT--CTCCATCCAGCAGAGAGAGAGAGAGAGAGAG 1061
DB 1654 TCTGTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1713
QY 1062 GTT 1064
DB 1714 TTT 1716

RESULT 14
US-08-450-393A-3
; Sequence 3, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Geert, Luann
; REGISTRATION NUMBER: 31, 822
; REFERENCE/DOCKET NUMBER: UCLL-237/020US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1979 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS

LOCATION: 81..1160
US-08-450-393A-3
Query Match 32.8%; Score 348.8; DB 1; Length 1979;
Best Local Similarity 61.5%; Pred. No. 4.6e-87;
Matches 636; Conservative 0; Mismatches 377; Indels 21; Gaps 4;
QY 37 ACCACATCTTACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 96
DB 141 ACCACCTTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 200
QY 97 ATGGCCAGCTTTGTCCTCCCGCTGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 156
DB 201 GGGGCCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 260
QY 157 GTGGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 216
DB 261 ATGCTGT 320
QY 217 CTGCTCAACCTGGCCATTTGCGACCTGCTCTCTGTCACCTTCCATCTGATGTCAC 276
DB 321 CTGCTCAACCTGGCCATTTGCGACCTGCTCTCTGTCACCTTCCATCTGATGTCAC 380
QY 277 TATGTCAGGGGCGATTAATCTGCTTTTGGCATGCGATGATGATGATGATGATGATGATG 336
DB 381 TCTG--CTGCAAAATGAGGGTCTTTGGGAATGCAATGTCAAATTAATTAACAGGGCTG 437
QY 337 TATGTCAGGGGCGATTTGCGACCTGCTCTCTGTCACCTTCCATCTGATGTCAC 396
DB 438 TATGTCAGGGGCGATTTGCGACCTGCTCTCTGTCACCTTCCATCTGATGTCAC 497
QY 397 CTGGCCATTTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 456
DB 498 CTGGCCATTTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 557
QY 457 ACCAGCATGTCACCTGCGGCTGCGATGTCAGCAGCTCTCTGATTTATCTGAT 516
DB 558 ACAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 617
QY 517 GAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 576
DB 618 AATGTCAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 669
QY 577 TATGTCAGGGGCGATTTGCGACCTGCTCTCTGTCACCTTCCATCTGATGTCAC 636
DB 670 ---GATGGAATTAATTTCCACACAAATATGAGAGAAATTTGGGCTGCTGCTGCTG 725
QY 637 CTGCTTATGCGATCTGTCACAGAGATGATGATGATGATGATGATGATGATGATGATG 696
DB 726 CTGCTTATGCGATCTGTCACAGAGATGATGATGATGATGATGATGATGATGATGATG 785
QY 697 AAAAAGT---ACAAGGCGATCGGCTGATTTTGTGATGATGATGATGATGATGATGATG 753
DB 786 AAGAGAGCATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 845
QY 754 TGAGCACCCTTAAGTGTGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 813
DB 846 TGAGCACCCTTAAGTGTGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 905
QY 814 GACTGTAGCGGAGCAGCATGTCGATGATGATGATGATGATGATGATGATGATGATGAT 873
DB 906 AACTGTGAAGGACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 965
QY 874 TCCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 933
DB 966 ACTGACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1025
QY 934 CTGCGCCATTTCTTCCAGAGGACCTGTCATGACCTGGGAGATATCCATCTCTCT 993
DB 1026 CTCTGCGTGTCTTCCGAAGGACATGACAGGCTTGTGCAAAATGTCAGTCTTTC 1085
QY 994 CCTAGTGAAGAGTGAAGA---ACCAGCTGTGCTCTGATGATGATGATGATGATGATGATG 1050

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Db 1086 TACAGGAGACAGTGGATGAGTACTTCAACAAACCCCTTCACATGGGGAGAGAGAA 1145
Qy 1051 CTCCTATTTGTT 1064
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Db 1146 GTCTGGCTGTT 1159

RESULT 15
US-08-446-669-3
: Sequence 3, Application US/08446669
: Patent No. 6132987
: GENERAL INFORMATION:
: APPLICANT: Charo, Israel
: APPLICANT: Coughlin, Shaun
: TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
: TITLE OF INVENTION: PROTEIN RECEPTORS
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
: STREET: 5 Palo Alto Square
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94306-2155
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/446,669
: FILING DATE: May 25, 1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Neeley, Richard
: REGISTRATION NUMBER: 30, 092
: REFERENCE/DOCKET NUMBER: USAL-237/01US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-843-5000
: TELEFAX: 415-857-0663
: TELEEX: 380816COOLEYPA
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1979 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 81..1160
: US-08-446-669-3

Query Match 32.8%; Score 348.8; DB 3; Length 1979;
Best Local Similarity 61.5%; Pred. No. 4.6e-87;
Matches 636; Conservative 0; Mismatches 377; Indels 21; Gaps 4;

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Db 321 CTGCTCAACCTGGCCATCTCTGATCTGCTTTTCTTATTACTCTCCCATTTGGGCTCAC 380
Qy 277 TATGTAGGGGGGCACTAGTGGGTTTGGCCATGGCATGTGAAGCTCCCTCAGGGTTT 336
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Db 381 TCTG---CTGCAATAGATGGGCTTTGGGAATGCAATGTGCAATTAATTCACAGGGCTG 437
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Qy 337 TATCACACAGGCTTTGATACAGCATCTTTTTCATATCTGCTGCAATTCAGAGGTAC 396
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 438 TATCATCATGGGTTATTTTGGCGGAATCTTCTTATCATCTCTCTGACATTCATATAC 497
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Qy 397 CTGGCCATTGTCATGCTGTGTTTGGCTTCAGAGCCCGGAGCTGTCACTTTTGGTGTCATC 456
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Db 498 CTGGCTATTTGTCATGCTGTGTTTGGCTTTAAAGCCAGAGCGGTACCTTTGGGGTG 557
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Qy 457 ACCAGATGTGACCTGGGGGCTGGAGGCTGTGACGCTTTCCTCAATTAATCTCTAT 516
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Db 558 ACAAGTGTATCACCTGGTTGGTGGCTGTGCTTGTGCTCCAGGAATCATCTTTACT 617
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Qy 517 GAGACTGAAGAGTGTGTTAAGAGACTTTTGCAGTGTCTTTACCAGAGATACAGTA 576
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Db 618 AATGGCAGAAAGAAATTTCTGTTTATGTCTGTGGCCCTTATTTCCAGAG----- 669
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Qy 577 TATAGCTGAGGCACTTTCACACTGTGAGAAATGACATCTTCTGTCTCTCCCTG 636
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Db 670 ---GATGAATTAATTTCCACACAAATATGAGGAACATTTTGGGGCTGTGCTGCGCTG 725
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Qy 637 CTGCTATGGCCATCTGCTACACAGGAATCATAAAGCTGTGAGTGCCCATATA 696
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Db 726 CTCTATATGCTCATCTGCACTGCGGAATCTGGAATCTGGAACCTGTGGGTGCAACGAG 785
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Qy 697 AAAAGT---ACAAAGCCATCCGCTCATTTTGTATCATGAGGCTGTGTTTCAATTTTC 753
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Db 786 AAGAAAGCATAGGCGATGAGAGATCTTACCATCATGATTTTACTTCTCTTC 845
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Qy 754 TGGACACCTTACATGTGCTATCTCTCTCTCTATCATCATCTTATTTGGAAT 813
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Db 846 TGGACTCCCTATTAACATTTGTCATCTCTGAAACACCTTCAGGAATTTCTGGGCTGAG 905
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Qy 814 GACTGTAGCGGAGCAAGCATCTGAGACCTGTATCTGTGACAGAGTATCGGCTAC 873
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Db 906 AACTGTGAAGACACAGTCACTGAGCAAGCCAGCAGGTGACAGACTCTTTGGGATG 965
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Qy 874 TCCCACTGTGATGAAACCCGATCTAGCCCTTTGTTGAGAGAGTTCCGGAATAC 933
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Db 966 ACTCATCTGCTGATCATATCCCATCATCTTATGCTTGTGTGGGAGAAAGTTACAGAA 1025
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Qy 934 CTGGGCCACTTCTTCCACAGGCACTTGTCTATGCACTGTGGGAGATPACATCCATTCTT 993
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Qy 994 CCTAGTGAAGAGCTGGAAGA---ACCAGCTGTGTCTTCCATCCACAGAGAGCGGAA 1050
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Qy 1051 CTCCTATTTGTT 1064
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Db 1146 GTCTGGCTGTT 1159

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Search completed: February 24, 2003, 14:25:21
Job time : 60.1378 secs

